## AMENDMENTS

**IN THE SPECIFICATION:**

Please replace paragraph [0010] on page 3, with the following rewritten paragraph:

[0010] Figure 2 (SEQ ID NO:2) shows a polypeptide sequence encoded by the nucleic acid of SEQ ID NO: 1.

Please replace paragraph [0013] on page 4, with the following rewritten paragraph:

[0013] Figure 5A shows a nucleotide sequence alignment for human PLA2G1B and related sequences from mouse, rat, and *P. obesus* (sand rat) (SEQ ID NOS:3-6). Figure 5B shows an amino acid sequence alignment between human PLA2G1B and related sequences from mouse, rat, and *P. obesus* (SEQ ID NOS:7-10). The human PLA2G1B amino acid sequence in Figure 5B has 148 amino acids and the mouse, rat, and *P. obesus* sequences have 146 amino acids. The human PLA2G1B amino acid sequence is 78% identical to the mouse sequence, 76% identical to the rat sequence, and 76% identical to the *P. obesus* sequence. The mouse sequence is 88% identical to the rat sequence and 77% identical to the *P. obesus* sequence, and the rat sequence is 80% identical to the *P. obesus* sequence.

Please replace paragraph [0242] on page 70, with the following rewritten paragraph:

[0242] The assay was carried out by first amplifying a region of interest in the sample by using a polymerase chain reaction (PCR) that incorporated the primers set forth in Table 2.

**Table 2**

| Reference SNP ID | Position in SEQ ID NO:1 | First PCR primer | SEQ ID NO: | Second PCR primer | SEQ ID NO: |
|---|---|---|---|---|---|
| rs2009391 | 4050 | TGC AGA GGC TCA ATC ACT GT | 11 | CAG GTG TGG TGG TGG ATT G | 12 |
| rs5631 | 4689 | CAC AGG CCA CAG CAA ACA G | 13 | TCA GAC TTG CAG GTT GAA AAA G | 14 |
| rs5632 | 6282 | GGC AGA CCG ATT TGA ACT CT | 15 | CGG GAT CAC GCA CTT GA | 16 |
| rs5633 | 6358 | GGC AGT TCC GCA AAA TGA T | 17 | TGC AGG CGG ATC ACT TAC TT | 18 |
| rs5634 | 7256 | AGC TGT CCC TCC CAC TTT C | 19 | GTG TGG GTG TAC GGG TTG T | 20 |
| rs5635 | 7300 | AGC TGT CCC TCC CAC TTT C | 21 | ATA GGT CAA GGA AGG GAT AAA C | 22 |
| rs5636 | 7301 | AGC TGT CCC TCC CAC TTT C | 23 | ATA GGT CAA GGA AGG GAT AAA C | 24 |
| rs5637 | 7328 | CAA GAA GCT GGA CAG CTG TA | 25 | ATA GGT CAA GGA AGG GAT AAA C | 26 |
| rs1186217 | 8062 | ATC ACC TCA ACC TCC GTT CA | 27 | GGT GGT GCA CGC TTG TAA TT | 28 |
| rs1179387 | 9182 | AAG GTA AGC AGA GAT ACG TAA ATT AT | 29 | GGT TAT CTT TGG GTA GTA GGA TTA TA | 30 |

Please replace paragraph [0244] beginning on page 70, with the following rewritten paragraph:

[0244] After the PCR reaction was completed, an extension oligonucleotide was hybridized to the PCR product. Extension oligonucleotides are reported in Table 3.

**Table 3**

| Position in SEQ ID NO:1 | Extension Oligonucleotide | |
|---|---|---|
| 4050 | TGA GAT GGG AGG ATC T (antisense) | (SEQ ID NO:31) |
| 4689 | ACT GGG AAC CTC GA (antisense) | (SEQ ID NO:32) |
| 6282 | GCT GAT GCC GCT G (antisense) | (SEQ ID NO:33) |
| 6358 | GGA GTG ACC CCT T | (SEQ ID NO:34) |

| Position in SEQ ID NO:1 | Extension Oligonucleotide | |
|---|---|---|
| 7256 | ACA CAT GAC AAC TGC TA | (SEQ ID NO:35) |
| 7300 | GGT GTG GGT GTA CGG (antisense) | (SEQ ID NO:36) |
| 7301 | GGT GTG GGT GTA CGG (antisense) | (SEQ ID NO:37) |
| 7328 | CCA CAC CTA TTC ATA CTC | (SEQ ID NO:38) |
| 8062 | CTT AGG CAG GAG AAT C (antisense) | (SEQ ID NO:39) |
| 9182 | GTA ATG CAA CTT CAA AC | (SEQ ID NO:40) |

Please replace paragraph [0247] beginning on page 71, with the following rewritten paragraph:

[0247] For each polymorphism, SpectroDESIGNER™ software (Sequenom, Inc.) was used to generate a set of PCR primers and a MassEXTEND™ primer was used to genotype the polymorphism. Table 4 shows PCR primers and Table 5 shows extension primers used for analyzing polymorphisms. The initial PCR amplification reaction was performed in a 5 μl total volume containing 1X PCR buffer with 1.5 mM $MgCl_2$ (Qiagen), 200 μM each of dATP, dGTP, dCTP, dTTP (Gibco-BRL), 2.5 ng of genomic DNA, 0.1 units of HotStar DNA polymerase (Qiagen), and 200 nM each of forward and reverse PCR primers specific for the polymorphic region of interest.

**Table 4**

| Reference SNP ID | Position in SEQ ID NO:1 | First PCR primer | SEQ ID NO: | Second PCR primer | SEQ ID NO: |
|---|---|---|---|---|---|
| rs2701632 | 436 | ACCCACTTAGCATCCT TCAG | 41 | TCTTATGTGGGTTCC TTGGG | 42 |
| rs2701631 | 839 | TGTGGCCATTGTGACT GAGA | 43 | GCCCGGGTGACAGA GTG | 44 |
| rs5633 | 6358 | TGTGGCAGTTCCGCAA AATG | 45 | AGTAGCAGCCGTAG TTGTTG | 46 |
| rs2070873 | 6653 | ACCCCGTTAGAGATGG AAAC | 47 | CTGTTGCTACATTCT GCCAC | 48 |
| rs5637 | 7328 | AATTTCTGCTGGACAA CCCG | 49 | CCTACTGCTACAGGT GATTG | 50 |
| rs1179387 | 9182 | CAAGCCAAAAGTAAT GCAAC | 51 | GGATTATAGATGCCT TCCAC | 52 |
| rs2066539 | 10164 | TCATCTCACACTGTAC TCTC | 53 | CAATATCCAAACAT GAGGTC | 54 |
| rs2701629 | 11649 | GACAGAGAGAGACAC TATCT | 55 | GAAATGCAAGCTGT TATTGG | 56 |

Please replace paragraph [0249] beginning on page 72, with the following rewritten paragraph:

[0249] Once the SAP reaction was complete, a primer extension reaction was initiated by adding a polymorphism-specific MassEXTEND™ primer cocktail to each sample. Each MassEXTEND™ cocktail included a specific combination of dideoxynucleotides (ddNTPs) and deoxynucleotides (dNTPs) used to distinguish polymorphic alleles from one another. In Table 5, ddNTPs are shown and the fourth nucleotide not shown is the dNTP (*e.g.*, in the first row A, C and G are ddNTPs and T is the dNTP).

**Table 5**

| Position in SEQ ID NO:1 | Extend Probe | SEQ ID NO: | Termination Mix |
|---|---|---|---|
| 436 | TTAGCATCCTTCAGGCCTAAA | 57 | A,C,G |
| 839 | GACTCTGCCTCAAAATAAATAAAA (antisense) | 58 | C,G,T |
| 6358 | GCCGTAGTTGTTGTATTCCAA (antisense) | 59 | A,C,T |
| 6653 | GTGCAAAACAGTGGGCGATGCT | 60 | A,C,T |
| 7328 | TGATTGCCGAGCCAGAGCA (antisense) | 61 | A,C,G |
| 9182 | TTTCCATAATAGATATTTATGTAG (antisense) | 62 | C,G,T |
| 10164 | CACTGTACTCTCCAATAAAGCACC | 63 | A,C,G |
| 11649 | CAAACAAACACACACACAAAAC | 64 | C,G,T |

Please replace paragraph [0261] on page 77, with the following rewritten paragraph:

[0261] The SNP at position 7256 of SEQ ID NO: 1 was also allelotyped and genotyped in NIDDM and non-NIDDM patients from the pool described above (see Example 4). The following PCR primers were used: ACGTTGGATGGGGTTGTCCAGCAGAAATTTAC (SEQ ID NO:65) (forward PCR primer) and ACGTTGGATGCTTTCCAGGTGCTGCCAG (SEQ ID NO:66) (reverse PCR primer); and AGACACATGACAACTGCTA (SEQ ID NO:67) (extend primer).

Please replace paragraph [0273] beginning on page 80, with the following rewritten paragraph:

[0273] Oligonucleotide primers were designed based upon the *P. obesus* sequence using Primer Express software (version 1.5), which was obtained at the http address docs.appliedbiosystems.com/pebiodocs/04303014.pdf. For PCR reactions, forward primers having the sequences GCTGTGTGGCAGTTCCGCAA; GTTCCGCAATATGATCAAGTGC; GATGAAACTCCTTCTGCTGGCTG; and SAAGATGAAACTCCTTCTGCTG (SEQ ID NOS:68-71) were utilized in conjunction with reverse primers having the sequences GGTGAAATAAGACAGCAAGG; GGAGAANCAGATGGCGGCCT; CGGTCACAGTTGCAGATGAAG; GGAAGTGGGGTGACAGCCTAACA (SEQ ID NOS:72-75); and GGTGACAGSCTAACAGWNTTTC (SEQ ID NO:76), where S is G or C; N is C, G, T, or A; and W is A or T. Also, another forward primer having the sequence 5'-GCACCCCAGTGGACGAATT-3' (SEQ ID NO:77) and a reverse primer having the sequence 5'-TCAGCCTCTTGGCCTTAGTGTAG-3'(SEQ ID NO:78) yielded an amplicon that was 70 base pairs in length and were used for RT-PCR. Primers for the endogenous control gene, cyclophilin, were designed based on the *P. obesus* sequence. Primer sequence specificity was confirmed by comparing the primer sequences against the GenBank nucleotide sequence for PLA2G1B using BLAST. Primers were synthesized at a 40 nmole concentration and purified by using a reverse-phase cartridge (GeneWorks, Australia).